



SEQUENCE LISTING

<110> Myers, Alan M.
James, Martha G.
<120> dull11 Coding for a Novel Starch Synthase and Uses
Thereof
<130> ISU-003BX
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<141> 2003-8-5
<150> US 09/554,467
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<223> cDNA sequence corresponding to the gene encoding the
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20      25      30

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35      40      45

Val Ile Arg Cys Val Val Ala Ser Pro Gly Cys Pro Asn Arg Lys
50      55      60

Ser Arg Thr Ala Ser Pro Asn Val Lys Val Ala Ala Tyr Ser Asn
65      70      75

Tyr Ala Pro Arg Leu Leu Val Glu Ser Ser Ser Lys Lys Ser Glu
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His His Asp Ser Ser Arg His Arg Glu Glu Thr Ile Asp Thr Tyr
95      100      105

Asn Gly Leu Ser Gly Ser Asp Ala Ala Glu Leu Thr Ser Asn Arg
110      115      120

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Thr	Ser	Gly	Ile	Val 170	Leu	Arg	Asn	Val	Ala 175	Val	Arg	Glu	Val	Asp 180
Pro	Lys	Asp	Glu	His 185	Asn	Ala	Lys	Asp	Val 190	Phe	Val	Val	Asp	Ser 195
Ser	Gly	Thr	Ala	Pro 200	Asp	Asn	Ala	Ala	Val 205	Glu	Glu	Val	Val	Asp 210
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Glu Thr Ser Gln	Lys 635	Thr Glu Gly Asp	Thr 640	Leu Gln Ala Thr	Phe 645
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Val Met Ile Glu	Glu 680	Gln Lys Ser Ile	Ala 685	Met Asn Glu Glu	Gln 690
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Ser Ser Trp Asp	Glu 725	Asn Glu Val Gly	Ile 730	Ile Glu Ala Asp	Glu 735
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Gly Gly Ile Tyr Asp Asn Arg Asn Gly Leu Asp Tyr His Ile Pro	1205	1210	1215
Val Phe Gly Ser Ile Ala Lys Glu Pro Pro Met His Ile Val His	1220	1225	1230
Ile Ala Val Glu Met Ala Pro Ile Ala Lys Val Gly Gly Leu Gly	1235	1240	1245
Asp Val Val Thr Ser Leu Ser Arg Ala Val Gln Asp Leu Gly His	1250	1255	1260
Asn Val Glu Val Ile Leu Pro Lys Tyr Gly Cys Leu Asn Leu Ser	1265	1270	1275
Asn Val Lys Asn Leu Gln Ile His Gln Ser Phe Ser Trp Gly Gly	1280	1285	1290
Ser Glu Ile Asn Val Trp Arg Gly Leu Val Glu Gly Leu Cys Val	1295	1300	1305
Tyr Phe Leu Glu Pro Gln Asn Gly Met Phe Gly Val Gly Tyr Val	1310	1315	1320
Tyr Gly Arg Asp Asp Asp Arg Arg Phe Gly Phe Phe Cys Arg Ser	1325	1330	1335
Ala Leu Glu Phe Leu Leu Gln Ser Gly Ser Ser Pro Asn Ile Ile	1340	1345	1350
His Cys His Asp Trp Ser Ser Ala Pro Val Ala Trp Leu His Lys	1355	1360	1365
Glu Asn Tyr Ala Lys Ser Ser Leu Ala Asn Ala Arg Val Val Phe	1370	1375	1380
Thr Ile His Asn Leu Glu Phe Gly Ala His His Ile Gly Lys Ala	1385	1390	1395
Met Arg Tyr Cys Asp Lys Ala Thr Thr Val Ser Asn Thr Tyr Ser	1400	1405	1410

Lys Glu Val Ser Gly His Gly Ala Ile Val Pro His Leu Gly Lys
 1415 1420 1425
 Phe Tyr Gly Ile Leu Asn Gly Ile Asp Pro Asp Ile Trp Asp Pro
 1430 1435 1440
 Tyr Asn Asp Asn Phe Ile Pro Val His Tyr Thr Cys Glu Asn Val
 1445 1450 1455
 Val Glu Gly Lys Arg Ala Ala Lys Arg Ala Leu Gln Gln Lys Phe
 1460 1465 1470
 Gly Leu Gln Gln Ile Asp Val Pro Val Val Gly Ile Val Thr Arg
 1475 1480 1485
 Leu Thr Ala Gln Lys Gly Ile His Leu Ile Lys His Ala Ile His
 1490 1495 1500
 Arg Thr Leu Glu Arg Asn Gly Gln Val Val Leu Leu Gly Ser Ala
 1505 1510 1515
 Pro Asp Ser Arg Ile Gln Ala Asp Phe Val Asn Leu Ala Asn Thr
 1520 1525 1530
 Leu His Gly Val Asn His Gly Gln Val Arg Leu Ser Leu Thr Tyr
 1535 1540 1545
 Asp Glu Pro Leu Ser His Leu Ile Tyr Ala Gly Ser Asp Phe Ile
 1550 1555 1560
 Leu Val Pro Ser Ile Phe Glu Pro Cys Gly Leu Thr Gln Leu Val
 1565 1570 1575
 Ala Met Arg Tyr Gly Thr Ile Pro Ile Val Arg Lys Thr Gly Gly
 1580 1585 1590
 Leu Phe Asp Thr Val Phe Asp Val Asp Asn Asp Lys Glu Arg Ala
 1595 1600 1605
 Arg Asp Arg Gly Leu Glu Pro Asn Gly Phe Ser Phe Asp Gly Ala
 1610 1615 1620
 Asp Ser Asn Gly Val Asp Tyr Ala Leu Asn Arg Ala Ile Ser Ala
 1625 1630 1635
 Trp Phe Asp Ala Arg Ser Trp Phe His Ser Leu Cys Lys Arg Val
 1640 1645 1650
 Met Glu Gln Asp Trp Ser Trp Asn Arg Pro Ala Leu Asp Tyr Ile
 1655 1660 1665
 Glu Leu Tyr Arg Ser Ala Ser Lys Leu
 1670

<210> 13
 <211> 60
 <212> PRT
 <213> maize
 <220>
 <221> 418..477
 <222> REPEAT
 <223> First 60 amino acid residue SBE-superrepeat of 180
 amino acid repeat residue in DU1.
 <400> 13

Asp Gln Ser Ile Ala Gly Ser His Arg Gln Asp Gln Ser Ile Ala

1	5	10	15
Gly Ala Pro Glu	Gln Ile Gln Ser Val	Ala Gly Tyr Ile Lys	Pro
	20	25	30
Asn Gln Ser Ile	Val Gly Ser Cys Lys	Gln His Glu Leu Ile	Ile
	35	40	45
Pro Glu Pro Lys	Lys Ile Glu Ser Ile	Ile Ser Tyr Asn Glu	Ile
	50	55	60
<210>	14		
<211>	60		
<212>	PRT		
<213>	maize		
<220>			
<222>	REPEAT		
<221>	478..537		
<223>	Second 60 amino acid residue SBE-superrepeat of 180 amino acid repeat residue in DU1.		
<400>	14		
Asp Gln Ser Ile	Val Gly Ser His Lys	Gln Asp Lys Ser Val	Val
1	5	10	15
Ser Val Pro Glu	Gln Ile Gln Ser Ile	Val Ser His Ser Lys	Pro
	20	25	30
Asn Gln Ser Thr	Val Pro Ser Tyr Arg	Gln Ala Glu Ser Ile	Ile
	35	40	45
Gly Val Pro Glu	Lys Val Gln Ser Ile	Thr Ser Tyr Asp Lys	Leu
	50	55	60
<210>	15		
<211>	60		
<212>	PRT		
<213>	maize		
<220>			
<222>	REPEAT		
<221>	438..597		
<223>	Third 60 amino acid residue SBE-superrepeat of 180 amino acid repeat residue in DU1.		
<400>	15		
Asp Gln Ser Ile	Val Gly Ser Leu Lys	Gln Asp Glu Pro Ile	Ile
1	5	10	15
Ser Val Pro Glu	Lys Ile Gln Ser Ile	Val His Tyr Thr Lys	Pro
	20	25	30
Asn Gln Ser Ile	Val Gly Leu Pro Lys	Gln Gln Gln Ser Ile	Val
	35	40	45
His Ile Val Glu	Pro Lys Gln Ser Ile	Asp Gly Phe Pro Lys	Gln
	50	55	60
<210>	16		
<211>	10		
<212>	PRT		
<213>	maize		
<220>			
<221>	478..487		
<222>	REPEAT		
<223>	Sequence of SBE-repeat in DU1.		
<400>	16		
Asp Gln Ser Ile	Val Gly Ser His Lys	Gln	
1	5	10	
<210>	17		

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        <211>    10
        <212>    PRT
        <213>    maize
        <220>
        <221>    538..547
        <222>    REPEAT
        <223>    Sequence of SBE-repeat in DU1.
        <400>    17
Asp Gln Ser Ile Val Gly Ser Leu Lys Gln
1          5          10
        <210>    18
        <211>    10
        <212>    PRT
        <213>    maize
        <220>
        <221>    448.457
        <222>    REPEAT
        <223>    Sequence of SBE-repeat in DU1.
        <400>    18
Asn Gln Ser Ile Val Gly Ser Cys Lys Gln
1          5          10
        <210>    19
        <211>    10
        <212>    PRT
        <213>    maize
        <220>
        <221>    568..577
        <222>    REPEAT
        <223>    Sequence of SBE-repeat in DU1.
        <400>    19
Asn Gln Ser Ile Val Gly Leu Pro Lys Gln
1          5          10
        <210>    20
        <211>    10
        <212>    PRT
        <213>    maize
        <220>
        <221>    418..427
        <222>    REPEAT
        <223>    Sequence of SBE-repeat in DU1.
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Asp Gln Ser Ile Ala Gly Ser His Arg Gln
1          5          10
        <210>    21
        <211>    10
        <212>    PRT
        <213>    maize
        <220>
        <221>    428..437
        <222>    REPEAT
        <223>    Sequence of SBE-repeat in DU1.
        <400>    21
Asp Gln Ser Ile Ala Gly Ala Pro Glu Gln
1          5          10
        <210>    22
        <211>    10
        <212>    PRT
        <213>    maize
        <220>
        <221>    404..413
        <222>    REPEAT
        <223>    Sequence of SBE-repeat in DU1.

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    <400>      22
Asp Lys Ser Ile Val Gly Val Pro Gln Gln
 1              5              10

    <210>      23
    <211>      10
    <212>      PRT
    <213>      maize
    <220>
    <221>      598..607
    <222>      REPEAT
    <223>      Sequence of SBE-repeat in DU1.
    <400>      23
Asp Leu Ser Ile Val Gly Asn Glu Phe Gln
 1              5              10

    <210>      24
    <211>      25
    <212>      PRT
    <213>      maize
    <220>
    <221>      529..553
    <222>      REPEAT
    <223>      Conserved M-box sequence in maize SBEI.
    <400>      24
Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly
 1              5              10              15

Asp Lys Thr Ile Ala Phe Leu Leu Met Asp
              20              25

    <210>      25
    <211>      25
    <212>      PRT
    <213>      pea
    <220>
    <221>      529..553
    <222>      REPEAT
    <223>      Conserved M-box sequence in pea SBEII.
    <400>      25
Lys Cys Val Ser Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly
 1              5              10              15

Asp Lys Thr Ile Ala Phe Leu Leu Met Asp
              20              25

    <210>      26
    <211>      25
    <212>      PRT
    <213>      wheat
    <220>
    <221>      529..553
    <222>      REPEAT
    <223>      Conserved M-box sequence in wheat SBEI.
    <400>      26
Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ser Ile Val Gly
 1              5              10              15

Asp Lys Thr Met Ala Phe Leu Leu Met Asp
              20              25

    <210>      27
    <211>      25
    <212>      PRT
    <213>      maize
    <220>

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<221> 572..596
<222> REPEAT
<223> Conserved M-box sequence in maize SBEIa.
<400> 27
Lys Cys Val Thr Tyr Cys Glu Ser His Asp Gln Ala Leu Val Gly
 1          5          10          15

Asp Lys Thr Ile Ala Phe Trp Leu Met Asp
          20          25

<210> 28
<211> 15
<212> PRT
<213> maize
<220>
<221> 572..596
<222> REPEAT
<223> Conserved M-box sequence in maize SBEIIb.
<400> 28
Lys Cys Val Thr Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly
 1          5          10          15

<210> 29
<211> 25
<212> PRT
<213> pea
<220>
<221> 572..596
<222> REPEAT
<223> Conserved M-box sequence in pea SBEI.
<400> 29
Lys Cys Val Val Tyr Cys Glu Ser His Asp Gln Ala Leu Val Gly
 1          5          10          15
Asp Lys Thr Met Ala Phe Leu Leu Met Asp
          20          25

<210> 30
<211> 25
<212> PRT
<213> yeast
<220>
<221> 477..501
<222> REPEAT
<223> Conserved M-box sequence in yeast GLC3 glycogen
        synthase.
<400> 30
Lys Val Val Ala Tyr Cys Glu Ser His Asp Gln Ala Leu Val Gly
 1          5          10          15
Asp Lys Ser Leu Ala Phe Trp Leu Met Asp
          20          25

<210> 31
<211> 25
<212> PRT
<213> Homo sapiens
<220>
<221> 477..501
<222> REPEAT
<223> Conserved M-box sequence in human liver glycogen
        synthase.
<400> 31
Lys Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly
 1          5          10          15

Asp Lys Thr Leu Ala Phe Trp Leu Met Asp
          20          25

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<210> 32
<211> 28
<212> PRT
<213> maize
<220>
<221> 150..177
<222> REPEAT
<223> Second 28 amino acid residue repeat of 85 residue
repeat in N-terminus of DU1.
<400> 32
Glu Thr Val Asp Glu Ala Glu Val Glu Glu Asp Lys Phe Glu Val
 1          5          10          15
Asp Thr Ser Gly Ile Val Leu Arg Asn Val Ala Val Arg
          20          25

<210> 33
<211> 29
<212> PRT
<213> artificial sequence
<220>
<221> 178..205
<222> REPEAT
<223> Second 28 amino acid residue repeat of 85 residue
repeat in N-terminus of DU1.
<400> 33
Glu Val Asp Pro Lys Asp Glu His Asn Ala Lys Asp Val Phe Val
 1          5          10          15
Val Asp Ser Ser Gly Thr Ala Pro Asp Asn Ala Ala Val Glu
          20          25

<210> 34
<211> 27
<212> PRT
<213> maize
<220>
<221> 206..233
<222> REPEAT
<223> Third 28 amino acid residue repeat of 85 residue
repeat in N-terminus of DU1.
<400> 34
Glu Val Val Asp Glu Ala Glu Val Glu Glu Asp Met Val Asp Val
 1          5          10          15
Asp Ile Leu Gly Leu Asp Leu Asn Asn Ala Thr Ile
          20          25

<210> 35
<211> 1230
<212> PRT
<213> potato
<220>
<223> Deduced amino acid sequence of potato starch synthase
SSIII.
<400> 35
Met Asp Val Pro Phe Pro Leu His Arg Ser Leu Ser Cys Thr Ser
 1          5          10          15
Val Ser Asn Ala Ile Thr His Leu Lys Ile Lys Pro Ile Leu Gly
          20          25          30
Phe Val Ser His Gly Thr Thr Ser Leu Ser Val Gln Ser Ser Ser
          35          40          45
Trp Arg Lys Asp Gly Met Val Thr Gly Val Ser Phe Ser Ile Cys
          50          55          60

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Ala	Asn	Phe	Ser	Gly	Arg	Arg	Arg	Arg	Lys	Val	Ser	Thr	Pro	Arg	
				65					70					75	
Ser	Gln	Gly	Ser	Ser	Pro	Lys	Gly	Phe	Val	Pro	Arg	Lys	Pro	Ser	
				80					85					90	
Gly	Met	Ser	Thr	Gln	Arg	Lys	Val	Gln	Lys	Ser	Asn	Gly	Asp	Lys	
				95					100					105	
Glu	Ser	Lys	Ser	Thr	Ser	Thr	Ser	Lys	Glu	Ser	Glu	Ile	Ser	Asn	
				110					115					120	
Gln	Lys	Thr	Val	Glu	Ala	Arg	Val	Glu	Thr	Ser	Asp	Asp	Asp	Thr	
				125					130					135	
Lys	Gly	Val	Val	Arg	Asp	His	Lys	Phe	Leu	Glu	Asp	Glu	Asp	Glu	
				140					145					150	
Ile	Asn	Gly	Ser	Thr	Lys	Ser	Ile	Ser	Met	Ser	Pro	Val	Arg	Val	
				155					160					165	
Ser	Ser	Gln	Phe	Val	Glu	Ser	Glu	Glu	Thr	Gly	Gly	Asp	Asp	Lys	
				170					175					180	
Asp	Ala	Val	Lys	Leu	Asn	Lys	Ser	Lys	Arg	Ser	Glu	Glu	Ser	Gly	
				185					190					195	
Phe	Ile	Ile	Asp	Ser	Val	Ile	Arg	Glu	Gln	Ser	Gly	Ser	Gln	Gly	
				200					205					210	
Glu	Thr	Asn	Ala	Ser	Ser	Lys	Gly	Ser	His	Ala	Val	Gly	Thr	Lys	
				215					220					225	
Leu	Tyr	Glu	Ile	Leu	Gln	Val	Asp	Val	Glu	Pro	Gln	Gln	Leu	Lys	
				230					235					240	
Glu	Asn	Asn	Ala	Gly	Asn	Val	Glu	Tyr	Lys	Gly	Pro	Val	Ala	Ser	
				245					250					255	
Lys	Leu	Leu	Glu	Ile	Thr	Lys	Ala	Ser	Asp	Val	Glu	His	Thr	Glu	
				260					265					270	
Ser	Asn	Glu	Ile	Asp	Asp	Leu	Asp	Thr	Asn	Ser	Phe	Phe	Lys	Ser	
				275					280					285	
Asp	Leu	Ile	Glu	Glu	Asp	Glu	Pro	Leu	Ala	Ala	Gly	Thr	Val	Glu	
				290					295					300	
Thr	Gly	Asp	Ser	Ser	Leu	Asn	Leu	Arg	Leu	Glu	Met	Glu	Ala	Asn	
				305					310					315	
Leu	Arg	Arg	Gln	Ala	Ile	Glu	Arg	Leu	Ala	Glu	Glu	Asn	Leu	Leu	
				320					325					330	
Gln	Gly	Ile	Arg	Leu	Phe	Cys	Phe	Pro	Glu	Val	Val	Lys	Pro	Asp	
				335					340					345	
Glu	Asp	Val	Glu	Ile	Phe	Leu	Asn	Arg	Gly	Leu	Ser	Thr	Leu	Lys	
				350					355					360	
Asn	Glu	Ser	Asp	Val	Leu	Ile	Met	Gly	Ala	Phe	Asn	Glu	Trp	Arg	
				365					370					375	

Tyr	Arg	Ser	Phe	Thr 380	Thr	Arg	Leu	Thr	Glu 385	Thr	His	Leu	Asn	Gly 390
Asp	Trp	Trp	Ser	Cys 395	Lys	Ile	His	Val	Pro 400	Lys	Glu	Ala	Tyr	Arg 405
Ala	Asp	Phe	Val	Phe 410	Phe	Asn	Gly	Gln	Asp 415	Val	Tyr	Asp	Asn	Asn 420
Asp	Gly	Asn	Asp	Phe 425	Ser	Ile	Thr	Val	Lys 430	Gly	Gly	Met	Gln	Ile 435
Ile	Asp	Phe	Glu	Asn 440	Phe	Leu	Leu	Glu	Glu 445	Lys	Trp	Arg	Glu	Gln 450
Glu	Lys	Leu	Ala	Lys 455	Glu	Gln	Ala	Glu	Arg 460	Glu	Arg	Leu	Ala	Glu 465
Glu	Gln	Arg	Arg	Ile 470	Glu	Ala	Glu	Lys	Ala 475	Glu	Ile	Glu	Ala	Asp 480
Arg	Ala	Gln	Ala	Lys 485	Glu	Glu	Ala	Ala	Lys 490	Lys	Lys	Lys	Val	Leu 495
Arg	Glu	Leu	Met	Val 500	Lys	Ala	Thr	Lys	Thr 505	Arg	Asp	Ile	Thr	Trp 510
Tyr	Ile	Glu	Pro	Ser 515	Glu	Phe	Lys	Cys	Glu 520	Asp	Lys	Val	Arg	Leu 525
Tyr	Tyr	Asn	Lys	Ser 530	Ser	Gly	Pro	Leu	Ser 535	His	Ala	Lys	Asp	Leu 540
Trp	Ile	His	Gly	Gly 545	Tyr	Asn	Asn	Trp	Lys 550	Asp	Gly	Leu	Ser	Ile 555
Val	Lys	Lys	Leu	Val 560	Lys	Ser	Glu	Arg	Ile 565	Asp	Gly	Asp	Trp	Trp 570
Tyr	Thr	Glu	Val	Val 575	Ile	Pro	Asp	Gln	Ala 580	Leu	Phe	Leu	Asp	Trp 585
Val	Phe	Ala	Asp	Gly 590	Pro	Pro	Lys	His	Ala 595	Ile	Ala	Tyr	Asp	Asn 600
Asn	His	Arg	Gln	Asp 605	Phe	His	Ala	Ile	Val 610	Pro	Asn	His	Ile	Pro 615
Glu	Glu	Leu	Tyr	Trp 620	Val	Glu	Glu	Glu	His 625	Gln	Ile	Phe	Lys	Thr 630
Leu	Gln	Glu	Glu	Arg 635	Arg	Leu	Arg	Glu	Ala 640	Ala	Met	Arg	Ala	Lys 645
Val	Glu	Lys	Thr	Ala 650	Leu	Leu	Lys	Thr	Glu 655	Thr	Lys	Glu	Arg	Thr 660
Met	Lys	Ser	Phe	Leu 665	Leu	Ser	Gln	Lys	His 670	Val	Val	Tyr	Thr	Glu 675
Pro	Leu	Asp	Ile	Gln 680	Ala	Gly	Ser	Ser	Val 685	Thr	Val	Tyr	Tyr	Asn 690
Pro	Ala	Asn	Thr	Val 695	Leu	Asn	Gly	Lys	Pro 700	Glu	Ile	Trp	Phe	Arg 705

Cys	Ser	Phe	Asn	Arg	Trp	Thr	His	Arg	Leu	Gly	Pro	Leu	Pro	Pro	
				710					715					720	
Gln	Lys	Met	Ser	Pro	Ala	Glu	Asn	Gly	Thr	His	Val	Arg	Ala	Thr	
				725					730					735	
Val	Lys	Val	Pro	Leu	Asp	Ala	Tyr	Met	Met	Asp	Phe	Val	Phe	Ser	
				740					745					750	
Glu	Arg	Glu	Asp	Gly	Gly	Ile	Phe	Asp	Asn	Lys	Ser	Gly	Met	Asp	
				755					760					765	
Tyr	His	Ile	Pro	Val	Phe	Gly	Gly	Val	Ala	Lys	Glu	Pro	Pro	Met	
				770					775					780	
His	Ile	Val	His	Ile	Ala	Val	Glu	Met	Ala	Pro	Ile	Ala	Lys	Val	
				785					790					795	
Gly	Gly	Leu	Gly	Asp	Val	Val	Thr	Ser	Leu	Ser	Arg	Ala	Val	Gln	
				800					805					810	
Asp	Leu	Asn	His	Asn	Val	Asp	Ile	Ile	Leu	Pro	Lys	Tyr	Asp	Cys	
				815					820					825	
Leu	Lys	Met	Asn	Asn	Val	Lys	Asp	Phe	Arg	Phe	His	Lys	Asn	Tyr	
				830					835					840	
Phe	Trp	Gly	Gly	Thr	Glu	Ile	Lys	Val	Trp	Phe	Gly	Lys	Val	Glu	
				845					850					855	
Gly	Leu	Ser	Val	Tyr	Phe	Leu	Glu	Pro	Gln	Asn	Gly	Leu	Phe	Ser	
				860					865					870	
Lys	Gly	Cys	Val	Tyr	Gly	Cys	Ser	Asn	Asp	Gly	Glu	Arg	Phe	Gly	
				875					880					885	
Phe	Phe	Cys	His	Ala	Ala	Leu	Glu	Phe	Leu	Leu	Gln	Gly	Gly	Phe	
				890					895					900	
Ser	Pro	Asp	Ile	Ile	His	Cys	His	Asp	Trp	Ser	Ser	Ala	Pro	Val	
				905					910					915	
Ala	Trp	Leu	Phe	Lys	Glu	Gln	Tyr	Thr	His	Tyr	Gly	Leu	Ser	Lys	
				920					925					930	
Ser	Arg	Ile	Val	Phe	Thr	Ile	His	Asn	Leu	Glu	Phe	Gly	Ala	Asp	
				935					940					945	
Leu	Ile	Gly	Arg	Ala	Met	Thr	Asn	Ala	Asp	Lys	Ala	Thr	Thr	Val	
				950					955					960	
Ser	Pro	Thr	Tyr	Ser	Gln	Glu	Val	Ser	Gly	Asn	Pro	Val	Ile	Ala	
				965					970					975	
Pro	His	Leu	His	Lys	Phe	His	Gly	Ile	Val	Asn	Gly	Ile	Asp	Pro	
				980					985					990	
Asp	Ile	Trp	Asp	Pro	Leu	Asn	Asp	Lys	Phe	Ile	Pro	Ile	Pro	Tyr	
				995					1000					1005	
Thr	Ser	Glu	Asn	Val	Val	Glu	Gly	Lys	Thr	Ala	Ala	Lys	Glu	Ala	
				1010					1015					1020	

Leu Gln Arg Lys Leu Gly Leu Lys Gln Ala Asp Leu Pro Leu Val
 1025 1030 1035
 Gly Ile Ile Thr Arg Leu Thr His Gln Lys Gly Ile His Leu Ile
 1040 1045 1050
 Lys His Ala Ile Trp Arg Thr Leu Glu Arg Asn Gly Gln Val Val
 1055 1060 1065
 Leu Leu Gly Ser Ala Pro Asp Pro Arg Val Gln Asn Asn Phe Val
 1070 1075 1080
 Asn Leu Ala Asn Gln Leu His Ser Lys Tyr Asn Asp Arg Ala Arg
 1085 1090 1095
 Leu Cys Leu Thr Tyr Asp Glu Pro Leu Ser His Leu Ile Tyr Ala
 1100 1105 1110
 Gly Ala Asp Phe Ile Leu Val Pro Ser Ile Phe Glu Pro Cys Gly
 1115 1120 1125
 Leu Thr Gln Leu Thr Ala Met Arg Tyr Gly Ser Ile Pro Val Val
 1130 1135 1140
 Arg Lys Thr Gly Gly Leu Tyr Asp Thr Val Phe Asp Val Asp His
 1145 1150 1155
 Asp Lys Glu Arg Ala Gln Gln Cys Gly Leu Glu Pro Asn Gly Phe
 1160 1165 1170
 Ser Phe Asp Gly Ala Asp Ala Gly Gly Val Asp Tyr Ala Leu Asn
 1175 1180 1185
 Arg Ala Leu Ser Ala Trp Tyr Asp Gly Arg Asp Trp Phe Asn Ser
 1190 1195 1200
 Leu Cys Lys Gln Val Met Glu Gln Asp Trp Ser Trp Asn Arg Pro
 1205 1210 1215
 Ala Leu Asp Tyr Leu Glu Leu Tyr His Ala Ala Arg Lys Leu Glu
 1220 1225 1230

<210> 36
 <211> 9
 <212> DNA
 <213> artificial sequence
 <220>
 <222> repeat_unit
 <223> Sequence of the nine base pair direct repeats flanking
 a Mui element in cloned fragment.
 <400> 36

gtgagaatg 9

<210> 37
 <211> 32
 <212> DNA
 <213> artificial sequence
 <221> primer
 <223> Primer containing restriction sites
 <400> 37

aaacccgggaattcgatggagatggctctacg